AMENDMENTS TO THE CLAIMS

Please amend claims 1, 3, 4, 8, 9, 12, 13, 23, 25, 26, 36, 38, and 80-81, and cancel claims 11, 44, 78, and 79 as set forth below.

The current listing of claims replaces all prior listings.

1. (Currently Amended) A method [to] for determin[e]ing the gender of a ~~canine~~ subject from the canis familiaris species, comprising:

a) contacting a nucleic acid sample from the ~~canine~~ subject with a first and a second oligonucleotide probe or primer, wherein the first and/or second oligonucleotide probe or primer is complementary to consensus regions between SEQ ID NO:22 and SEQ ID NO:23, and wherein such first and second probes or primers flank non-consensus regions between SEQ ID NO:22 and SEQ ID NO:23;

b) binding the first and second oligonucleotide probes or primers to the sample nucleic acid under conditions sufficient for hybridization of the probes or primers to the sample nucleic acid; and

c) detecting non-consensus regions which are specific to SEQ ID NO: 22 and/or specific to SEQ ID NO:23 in products resulting from the binding of step (b),

wherein detection of non-consensus regions which are specific to SEQ ID NO:22 and SEQ ID NO:23 correlates with the presence of X and Y chromosomal DNA of the species in the nucleic acid sample ~~at least one primer specific for a canine amelogenin gene, wherein one primer binds to a sequence of SEQ ID NO:22 and SEQ ID NO:23 and using the binding of the primers to detect a difference between the canine amelogenin gene on the Y chromosomes and the canine amelogenin gene on the X chromosome, thereby determining gender of the canine subject~~.

2. (Canceled)

3. (Currently Amended) The method of claim 1, further comprising determining ~~wherein gender of the canine subject is determined by observing~~ the presence of [an] amplified products as set forth in SEQ ID NO: 10 and SEQ ID NO:11.

4. (Currently Amended) The method of claim 3, ~~wherein gender of the canine subject is determined by contacting the nucleic acid sample with a primer pair,~~ wherein [a] the first oligonucleotide primer ~~of the primer pair~~ binds to SEQ ID NO:6 and SEQ ID NO:7 and [a] the second oligonucleotide primer ~~of the pair~~ binds to SEQ ID NO:8 and SEQ ID NO:9.

5. (Original) The method of claim 4, wherein the first primer comprises at least 10 nucleotides of SEQ ID NO:3 and the second primer comprises at least 10 nucleotides of SEQ ID NO:5.

6. (Original) The method of claim 5, wherein the first primer is SEQ ID NO:3 and the second primer is SEQ ID NO:5.

7. (Original) The method of claim 5, wherein the first primer is SEQ ID NO:4 and the second primer is SEQ ID NO:5.

8. (Currently Amended) The method of claim 5, wherein the oligonucleotide primers [pair] generate[s] [an] amplification products that [is a] are of different lengths, wherein a first length is indicative of a non-consensus region specific to SEQ ID NO:22 which correlates with ~~for the amelogenin gene on the~~ an X chromosome of the species and a second length is indicative of a non-consensus region specific to SEQ ID NO:23 which correlates with ~~the amelogenin gene on the~~ a Y chromosome of the species.

9. (Currently Amended) A method [to] for determin[e]ing the gender of a ~~canine~~ subject from the canis familiaris species, comprising:

a) contacting a nucleic acid sample from the ~~canine~~ subject with a first and a second oligonucleotide probe or primer, wherein the first and second oligonucleotide probes or primers comprise sequences which are complementary to non-consensus regions between SEQ ID NO:22 and SEQ ID NO:23;

b) binding the first and second oligonucleotide probes or primers to the sample nucleic acid under conditions sufficient for hybridization of the oligonucleotide probes or primers to the sample nucleic acid; and

c) detecting non-consensus regions which are specific to SEQ ID NO: 22 and/or specific to SEQ ID NO:23 in products resulting from the binding of step (b),
wherein failure to detect non-consensus regions which are specific to SEQ ID NO: 23 is indicative of the absence of Y chromosomal DNA of the species in the nucleic acid sample ~~at least one primer specific for a canine amelogenin gene, wherein one primer binds to a sequence of SEQ ID NO:22 and SEQ ID NO:23 and detecting binding of the at least one probe or primer, thereby determining gender of the canine subject~~.

10. (Canceled)

11. (Canceled)

12. (Currently Amended) The method of claim [11] 9, ~~wherein gender of the canine subject is determined by contacting the nucleic acid sample with a primer pair,~~ wherein a first oligonucleotide primer ~~of the primer pair~~ binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second oligonucleotide primer ~~of the primer pair~~ binds to SEQ ID NO:8 and/or SEQ ID NO:9.

13. (Currently Amended) The method of claim 9, wherein binding of the first and second ~~of the at least one~~ oligonucleotide probes or primers to non-consensus regions specific to SEQ ID NO:22 or specific to SEQ ID NO:23 distinguish[es] [the canine] an amelogenin gene of the species on [the] an X chromosome from [the] an amelogenin gene of the species on the Y chromosome in the sample.

Claims 14-22 (Canceled)

23. (Currently Amended) A method [to] of detecting binding of at least [one] two oligonucleotide primers to a canine amelogenin gene, wherein the at least [one] two oligonucleotide primers [binds] are complementary to a sequence of SEQ ID NO:22 and/or SEQ ID NO:23, comprising:

a) contacting a nucleic acid sample from a canine subject with the at least [one] two oligonucleotide primers ~~specific for~~ wherein the complementary regions flank non-consensus regions between SEQ ID NO:22 and SEQ ID NO:23;

b) binding the at least two oligonucleotide primers to the sample nucleic acid under conditions sufficient for hybridization of the oligonucleotide primers to the sample nucleic acid; and

c) detecting binding between the at least two oligonucleotide primers and the sample nucleic acid,

wherein detection of binding is indicative of the presence of homologous canine amelogenin sequences in the sample.

24. (Canceled)

25. (Currently Amended) The method of claim 23, wherein the ~~nucleic acid sample is contacted with~~ at least [one] two primers ~~pair that~~ generate[s] an amplification product as set forth in SEQ ID NO:10 or SEQ ID NO:11.

26. (Currently Amended) The method of claim 25, wherein a first primer of the at least two oligonucleotide primers is complementary ~~the nucleic acid sample is contacted with a primer pair, wherein a first primer of the pair binds~~ to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer is complementary ~~second primer of the primer pair binds~~ to SEQ ID NO:8 and/or SEQ ID NO:9.

Claims 27-35 (Canceled)

36. (Currently Amended) A method of [to] genotyping a ~~canine~~ canis familiaris subject, comprising:

a) contacting a nucleic acid sample from the ~~canine~~ canis familiaris subject with at least two sets of probes or primers, wherein the first set of probes or primers comprises first and second oligonucleotide probes or primers which are complementary to consensus regions between SEQ ID NO:22 and SEQ ID NO:23 and flank non-consensus regions between SEQ ID NO:22 and SEQ ID NO:23, and wherein the second set of probes or primers comprises third and fourth oligonucleotide probes or primers which are complementary to at least one microsatellite locus;

b) binding the probes or primers to the sample nucleic acid under conditions sufficient for hybridization of the probes or primers to the sample nucleic acid; and

c) detecting differences in products resulting from the binding of the probes or primers, wherein different products correlate with a particular genotype presented by the canis familiaris subject ~~at least primer specific for canine amelogenin, wherein one primer binds to a sequence of SEQ ID NO:22 and SEQ ID NO:23 and detecting binding of the at least one probe or primer, thereby genotyping the canine subject~~.

37. (Canceled)

38. (Currently Amended) The method of claim 36, wherein the first and second primers ~~nucleic acid sample is contacted with at least one primer pair that specifically binds~~ generate amplification products as set forth in SEQ ID NO:10 and[/or] SEQ ID NO:11.

Claims 39-43 (Canceled)

Claims 44-47 (Canceled)

48. (Original) The method of claim [44]36, wherein the microsatellite locus is at least one of PEZ1/CATA1, PEZ3, PEZ5, PEZ6, PEZ8, PEZ10, PEZ11, PEZ12, PEZ13, PEZ15, PEZ16, PEZ17, PEZ20, PEZ21, FH2010, FH2054, and FH2079.

Claims 49-77 (Canceled)

78. (Canceled)

79. (Canceled)

80. (Currently Amended) The method of any of claims 1[1]2, 25 or 38, wherein the first primer [pair] is SEQ ID NO:4 and the second primer is SEQ ID NO:5.

81. (Currently Amended) The method of any of claims 1[1]2, 25 or 38, wherein the first primer [pair] is SEQ ID NO:3 and the second primer is SEQ ID NO:5.